FILE Comp



Entrez

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 ▼ gap open: 11 gap extension: 1

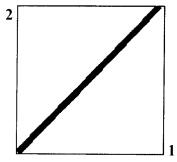
x dropoff: 30 expect: 10.000 wordsize: 3 Filter 🔽

Sequence 1 gi 829285 gluthamine synthetase [Pisum sativum]

Length 373 (1 .. 373)

Sequence 2 gi 404327 glutamate--ammonia ligase [Pinus sylvestris] Length 357 (1 .. 357)





NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 541 bits (1395), Expect = e-153Identities = 250/351 (19), Positives = 294/351 (838)

- Query: 7 DLLNLEITPFTDSIIAEYIWIGGTGIDVESESETISKPVSHPSEVPEWNYDGSSTGQAPG 66 DLLNLD++ T+ +IAEYIWI 3G+G+D+ESE+E++S PVS E+PEWNYDGSSTGOA G
- Sbjat: 7 DLLNLDLSDVTEKVIAEYIWIGGSGMDMRSKARSLSGPVSSVKELPKWNYDGSSTGQAQG 66
- Query: 67 EDSEVILYEQAIFKDPFRGGNNILWVGDAYTPAGEPIPTNKRHRAARIFSNPKVEARIPW 126 DSEVILYFÇAIF+DPFR G +ILV-CDAY+P G IP+NKR AA+IF+
- Sbjot: 67 HDSEVILYPÇAIFRDPFRRGKHILVICDAYSPNGTAIPSNKRAAAAKIFNEWAVSDBETW 126
- YG+EQEYTLLD +VFWPLGWP+
- DF++GRDI DAHYEAC+Y+GIN Sbjet: 127 YOLEQHYTLLQHDVKWPLGWPIGGYPÖPÇGFYUCGVGADHAWGFDIVDAHYHACLYSGIN 186
- Query: 187 ISGTNGEVMPGÇWEYÇVGPSVGTEAGDHIWASRYILERITEQAGVVLTLDPFP1EGLWNG 246
- ISG NGEVMPGQWE+QVGPSVG! A D +W +F+1+ERITE+AGVVL+ DPMPIEGDWNG Sbjct: 187 ISGINGEVMPGQWEFQVGPSVGISAADELWCAFFIMERITEKAGVVLSFDPKPIEGDWNG 246
- Query: 247 AGCHTNYSTKEMREDGGFEVIKKAILNLSLRHKIHIEAYGEGNERRLTGKHETASINDFS 306
- AGCHTNYSTKSMR++GGFEVIKKAI L LRHK HI AYGEGNERRLTG+HETA +N FS Sbjot: 247 AGCHTWYSTKSMRKEGGFEVIKKAIEKLKLRHKEHISAYGEGNERRLTGRHEDADMNTFS 396
- Query: 307 WGVANRGOSIRWGRDTEKNGKGYLEDREPASNMDFYVVTALLAESTLLWEP 357 WGVANRG S-RYGRDTEK GKGY EDRAPASNMDPY+VT+++AE+T+LW+P
- Sbjot: 30% WGVANRGASVRUGRDTEKEGKGYFEDRRPASHMDPYIVTSMIAETTILWKP 35%

CPU time: 0.09 user sets. 0.02 sys. sets 0.11 total sets.

```
K H
1.196 (1.416
Lambda
   0.315
Sapred
Lambda
           0.0410
   0.267
                     6.140
Matrix: BLOSUM62
Jap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1090
Number of Sequences: 0
Number of extensions: 73
Number of successful extensions: 2
Number if sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of ESP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 373
Tength of database: 445,599,717
effective HSP length: 128
effective length of query: 245
effective length of database: 445,599,589
offective search space: 109171899305
effective search space used: 109171899305
T: 9
A: 40
X1: 16 . 7.3 bits:
X2: 77 29.7 bits
X3: 77 (29.7 bits)
S1: 42 (22.0 bits)
S2: 75 (33.5 bits)
```



PubMed

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BLAST

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.5 [Nov-16-2002]

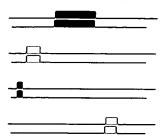
Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

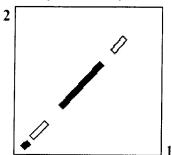
x_dropoff: 50 expect: 10.00(wordsize: 11 Filter **Align**

Sequence 1 gi 404326 P.sylvestris mRNA for glutamine synthetase

Length 1423 (1 .. 1423)

Sequence 2 gi 20752 Pea leaf mRNA for glutamine synthetase (EC 6.3.1.2) Length 1304 (1 .. 1304)





NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 160 bits (83), Expect = 66-36Identities = 285/386 (73)Strand = Plus / Plus

Query: 574 ototattbaggaatbaatatbagtggbatbaatggagaagtbatgbbagggbagtggg

Sbjct: 543 atatatgctggaattaacattagtggcaccaatggagaagttatgcctggacagtggg gluthamine synthetase 181 I Y A G I N I S G T N G E V M P G Q W

Query: 634 tittoaagtaggtosgtoagtgggtatotoagpagoagatgagotgtggtgtgctcgtt

```
Sbidt:
                                          KAS fathaagti ygtoomagigtaghtattyaagutggigalcatatotgggottoacggt
  gluthamine synthetase kul. Y _{	extsf{S}} V _{	extsf{S}} B _{	extsf{S}} V _{	extsf{S}} I _{	extsf{E}} A _{	extsf{S}} B _{	extsf{E}} W _{	extsf{A}} S _{	extsf{R}}
                                          694 attatggagaggattacagaaaaggoyggtgtogttmigtogittigatmocaagocaa
 Query:
                                                  The state of the the state of the territories and the state of the sta
                                          663 atomtigagagaattam gaabaagotygtgitgtgotbartotigatobaaaabbaa
 Sbjat:
 gluthamine synthetase 221 I L E R I T E Q A G V V L T L D P K P
 Query:
                                          T54 gagggggactggaatggtgctggatgccacacaaattacagcaccaagtccatgcgca
                                                  Sbjct:
                                          723 gagggtgattggaatggtgcaggatgtcacaccaattacagtacaaaqagcatgaggg
 gluthamine synthetase 241 E G D W N G A G C H T N Y S T K S M R
 Query:
                                          814 gagggaggcttcgaagtaattaagaa 839
                                                 Sbjct:
                                          783 gatggagggtttgaggtgataaagaa 808
 gluthamine synthetase 261 0 G G F E V I K K
 Score = 68.0 \text{ bits } (35), Expect = 4e-08
 Identities = 103/137 (\%5)
  Strand = Plus / Plus
Query:
                                         181 gagetteceaaatggaactatgaeggetecageactggaeaggeteaaggaeatgaea
                                                 Sbjct:
                                         150 gaggttcctaagtggaactatgatggatctagcactggacaagcccstggtgaagata
 gluthamine synthetase 50 \pm V P K W N Y D G S S T G Q A P G \pm D
⊉uery:
                                         241 gaagteattetatateeacaagetatetteegtgateeatttegeagaggaaageaca
                                                 Sbrat:
                                         210 gaagtgateetatateeteaageaatttteaaagateettteegtggeggaaacaata
gluthamine synthetase 70 E V I L Y P Q A I F K D P F R G G N N
Query:
                                         301 ttggtaatctgtgatgs 317
                                                 1:11: 1 1/1/1/1:
Sbict:
                                         270 ttggtcgtttgtgatgc 286
gluthamine synthetase 90 L V V C D A
Score = 52.6 \text{ bits } (27), Expect = 0.002
Identities = 43/51 (84.)
  Strand - Plus / Plus
Query:
                                         94 attgbagagtātatatggattggaggatbaggaatggatatgogbagtaaa 144
                                                tout. Then of different to single on thirty i.t.
Sbjct:
                                                attgotgagtacatatggattggtgggasaggaattyatgtgsgsagsaaa 113
gluthamine synthetase 21 I A E Y I W I G G T G I D V R S K
Score = 46.8 bits (24), Expect = 0.189
Identities = 84/114 (73.)
 Strand = Flus / Ilus
```

```
945 ötttttöttggggtgttgcaäatcgäggagettcagttägagtgggcogggacacaga
Query:
                          aidial (IDII I) it it II ili alt i latiti i vitti il
Sbrot:
                     914
                          cttttcttggggagtggctaaccggggatgctcaatccgtgtgggaagagacaccga
pluthamine synthetase 305
                          F S W G V A N R G C S I R V G R D T E
luery:
                     1005 agaaggaaaaggttattttgaggaccgtcgacctgcttcaaacatggatccata 10
                           3bist:
                     974
                          gaatggcaaaggttacttggaagacaggcgtccgqcttcqaacatqqatccata 10
gluthamine synthetase 325
                          N 3 K G Y L E D R R P A S N M D P Y
CPU time:
            0.03 user secs.
                                 0.07 sys. secs
                                                        0.15 total secs.
Lamina
    1.3
           0.621
Sapped
Lambia
          0.621
   1.37
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number | f successful extensions: 5
Number f sequences perter than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of H2P's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 4
length of query: 1423
length of database: 7,976,531,563
effective H3P length: 25
effective length of query: 1398
effective length of database: 7,976,831,538
effective search space: 11151191090124
effective search space used: 11151191090124
7: 0
A: 0
%1: → (11.5 bits)
X2: 26 50.0 bits:
S1: 12 23.8 bits
$2: 21 (41.1 bits)
```